

cacgagggaacaacctctctctscagcagagagtgacacctgctttaggaccatcaagctctgctaactgaatc -474  
 tcacctaattgcaggatcacattgcaaagctttcactctttcccacctgcttggtggtgaaatctctctgcggaatc -395  
 tcagaaagtaagttccatcctgagaatatttcacaaagaatttccttaagagctggactgggtcttgacccctggaat -316  
 ttaagaaattcttaagacaatgtcaaataatgatccaagagaaaatgtgatttgagctgagacaattgtgcatatcg -237  
 tctaataataaaaaccatactagcctatagaaaacaatatttgaataataaaaaccatactagcctatagaaaacaa, -158  
 tatttgaaagattgctaccactaaaaagaaaactactacaacttgacaagactgctgcaaacttcaattgggtcaccaca -79  
 acttgacaaggttgctataaaaacaagattgctacaacttctagtttatgttatacagcatatttcatttgggcttaatg -1

atg gag aaa aag tgt acc ctg tat ttt ctg gtt ctc ttg cct ttt ttt atg att ctt gtt  
 1 M E K K C T L Y F L V L L P F F M I L V 60  
 aca gca gaa tta gaa gag agt cct gag gac tca att cag ttg gga gtt act aga aat aaa  
 21 T A E L E E S P E D S I Q L G V T R N K 120  
 atc atg aca gct caa tat gaa tgt tac caa aag att atg caa gac ccc att caa caa gca  
 41 I M T A Q Y E C Y Q K I M Q D P I Q Q A 180  
 gaa ggc gtt tac tgc aac aga acc tgg gat gga tgg ctc tgc tgg aac gat gtt gca gca  
 61 E G V Y C N R T W D G W L C W N D V A A 240  
 gga act gaa tca atg cag ctc tgc cct gat tac ttt cag gac ttt gat cca tca gaa aaa  
 81 G T E S M Q L C P D Y F Q D F D P S E K 300  
 gtt aca aag atc tgt gac caa gat gga aac tgg ttt aga cat cca gca agc aac aga aca  
 101 V T K I C D Q D G N W F R H P A S N R T 360  
 tgg aca aat tat acc cag tgt aat gtt aac acc cac gag aaa gtg aag act gca cta aat  
 121 W T N Y T Q C N V N T H E K V K T A L N 420  
 ttg ttt tac ctg acc ata att gga cac gga ttg tct att gca tca ctg ctt atc tcg ctt  
 141 L F Y L T I I G H G L S I A S L L I S L 480  
 ggc ata ttc ttt tat ttc aag agc cta agt tgc caa agg att acc tta cac aaa aat ctg  
 161 G I F F Y F K S L S C Q R I T L H K N L 540  
 ttc ttc tca ttt gtt tgt aac tct gtt gta aca atc att cac ctc act gca gtg gcc aac  
 181 F F S F V C N S V V T I I H L T A V A N 600  
 aac cag gcc tta gta gcc aca aat cct gtt agt tgc aaa gtg tcc cag ttc att cat ctt  
 201 N Q A L V A T N P V S C K V S Q F I H L 660  
 tac ctg atg ggc tgt aat tac ttt tgg atg ctc tgt gaa ggc att tac cta cac aca ctc  
 221 Y L M G C N Y F W M L C E G I Y L H T L 720  
 att gtg gtg gcc gtg ttt gca gag aag caa cat tta atg tgg tat tat ttt ctt ggc tgg  
 241 I V V A V F A E K Q H L M W Y Y F L G W 780  
 gga ttt cca ctg att cct gct tgt ata cat gcc att gct aga agc tta tat tac aat gac  
 261 G F P L I P A C I H A I A R S L Y Y N D 840  
 aat tgc tgg atc agt tct gat acc cat ctc ctc tac att atc cat ggc cca att tgt gct  
 281 N C W I S S D T H L L Y I I H G P I C A 900  
 gct tta ctg gtg aat ctt ttt ttc ttg tta aat att gta cgc gtt ctc atc acc aag tta  
 300 A L L V N L F F L L N I V R V L I T K L 960  
 aaa gtt aca cac caa gcg gaa tcc aat ctg tac atg aaa gct gtg aga gct act ctt atc  
 321 K V T H Q A E S N L Y M K A V R A T L I 1020

FIG. 1A

ttg gtg cca ttg ctt ggc att gaa ttt gtg ctg att cca tgg cga cct gaa gga aag att  
 341 L V P L L G I E F V L I P W R P E G K I 1080  
 gca gag gag gta tat gac tac atc atg cac atc ctt atg cac ttc cag ggt ctt ttg gtc  
 381 A E E V Y D Y I M H I L M H F Q G L L V 1140  
 tct acc att ttc tgc ttc ttt aat gga gag gtt caa gca att ctg aga aga aac tgg aat  
 401 S T I F C F F N G E V Q A I L R R N W N 1200  
 caa tac aaa atc caa ttt gga aac agc ttt tcc aac tca gaa gct ctt cgt agt gcg tct  
 421 Q Y K I Q F G N S F S N S E A L R S A S 1260  
 tac aca gtg tca aca atc agt gat ggt cca ggt tat agt cat gac tgt cct agt gaa cac  
 441 Y T V S T I S D G P G Y S H D C P S E H 1320  
 tta aat gga aaa agc atc cat gat att gaa aat gtt ctc tta aaa cca gaa aat tta tat  
 462 L N G K S I H D I E N V L L K P E N L Y 1380  
 aat tga aaatagaaggatgggtgtctcactgtttggtgcttctcctaactcaaggacttggacccatgactctgtag  
 N  
 ccagaagacttcaatattaaatgactttggggaatgtcataaagaagagccttcacatgaaattagtagtgtgttgata 1536  
 agagtgtaacatccagctctatgtgggaaaaaagaaatcctgggttgtaattgtttgtcagtaaatactcccactatgcc 1615  
 tgatgtgacgctactaacctgacatcaccaagtgtggaattggagaaaagcacaatcaacttttctgagctggtgtaag 1694  
 ccagttccagcacaccattgatgaattcaacaaatggctgtaaaactaaacatacatgttgggcatgattctaccctt 1773  
 attcscaccaagagacctagctaaggtctataaacatgaagggaaaattagcttttagttttaaaactctttatcccat 1852  
 cttgattggggcagttgactttttttttccagagtgcctgtctctttttgtaactaccctctcaaatggacaata 1931  
 ccagaagtgaattatccctgctggctttctttctctatgaaaagcaactgagtacaattgttatgatctactcatttg 2010  
 ctgacacatcagttatatcttggcatatccattgtggaaactggatgaacaggatgtataatatgcaatcttacttc 2089  
 tatatcattagggaaaacatcttagttgatgtacaaaacacctgtcaacctcttctgtcttaccaaacagtgagg 2168  
 gaattcctagctgtaaatataaattttgcccttccatttctactgtataaacaattagcaatcattttatataaagaa 2247  
 aatcaatgaaggatttcttattttcttggaaattttgtaaaaagaaattgtgaaaaatgagcttgtaataactccattat 2326  
 tttattttatagtctcaaatcaatacatacaacctatgtaatttttaagcaaatatataatgaacaatgtgtgtat 2405  
 gttaatatctgatactgtatctgggctgatttttaataaaatagagtctggaatgctaaaaaaaaaaaaaaaaa 2481

FIG. 1B

[illegible]

FIG. 2

FIG. 3

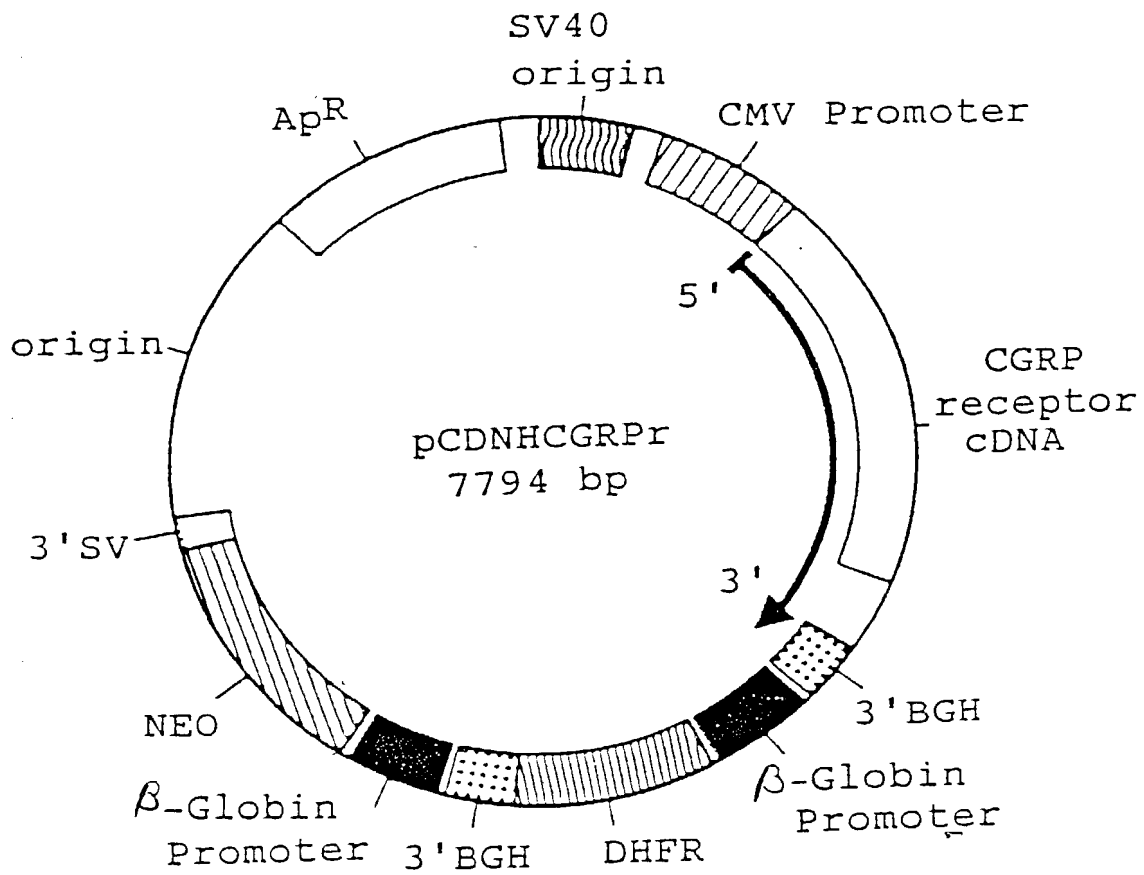
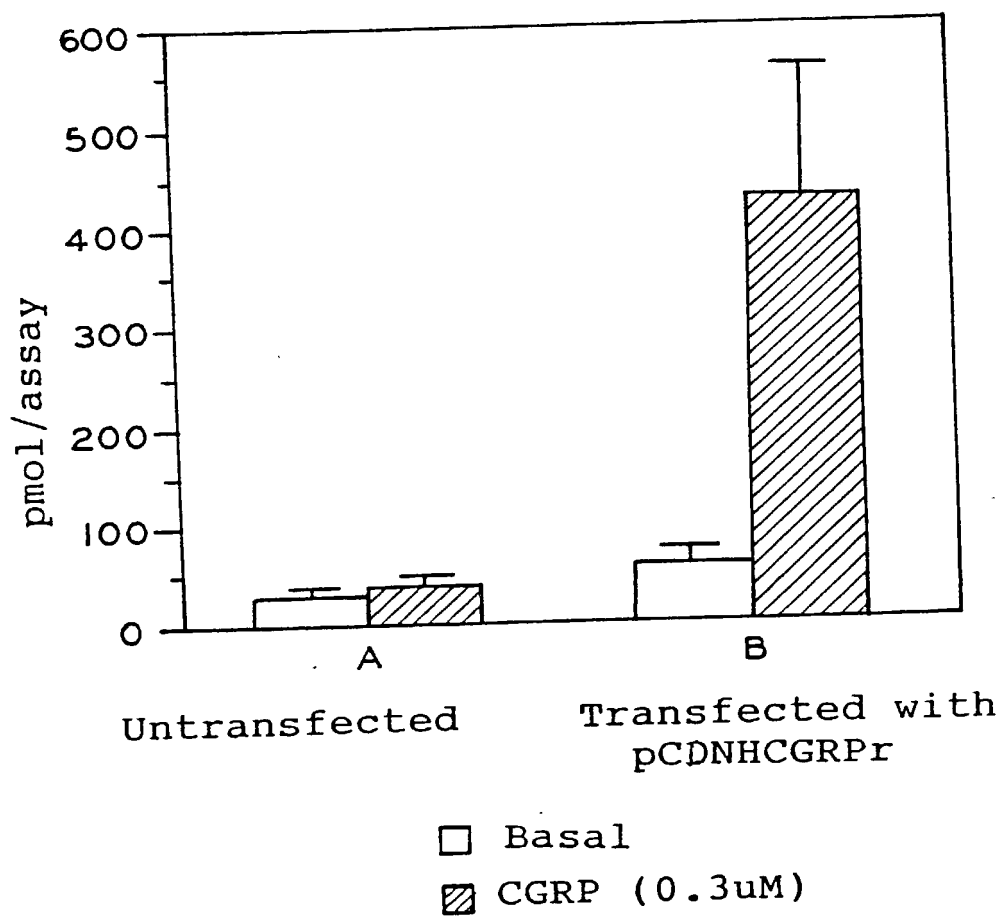


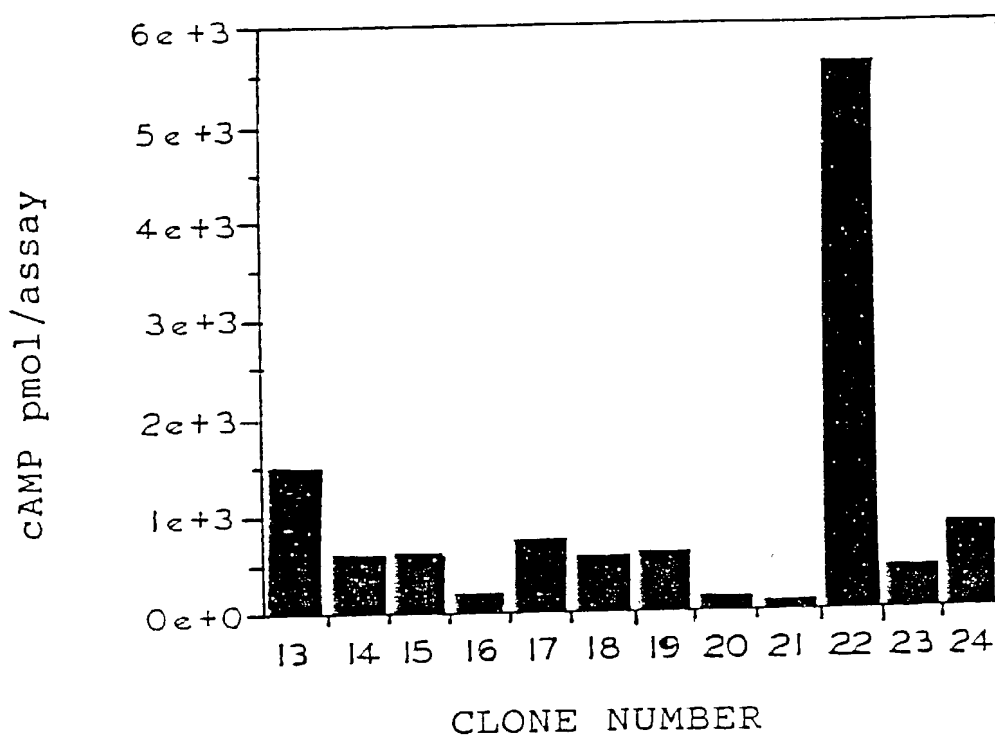
FIG. 4

CAMP RESPONSE IN 293 CELLS



# FIG. 5

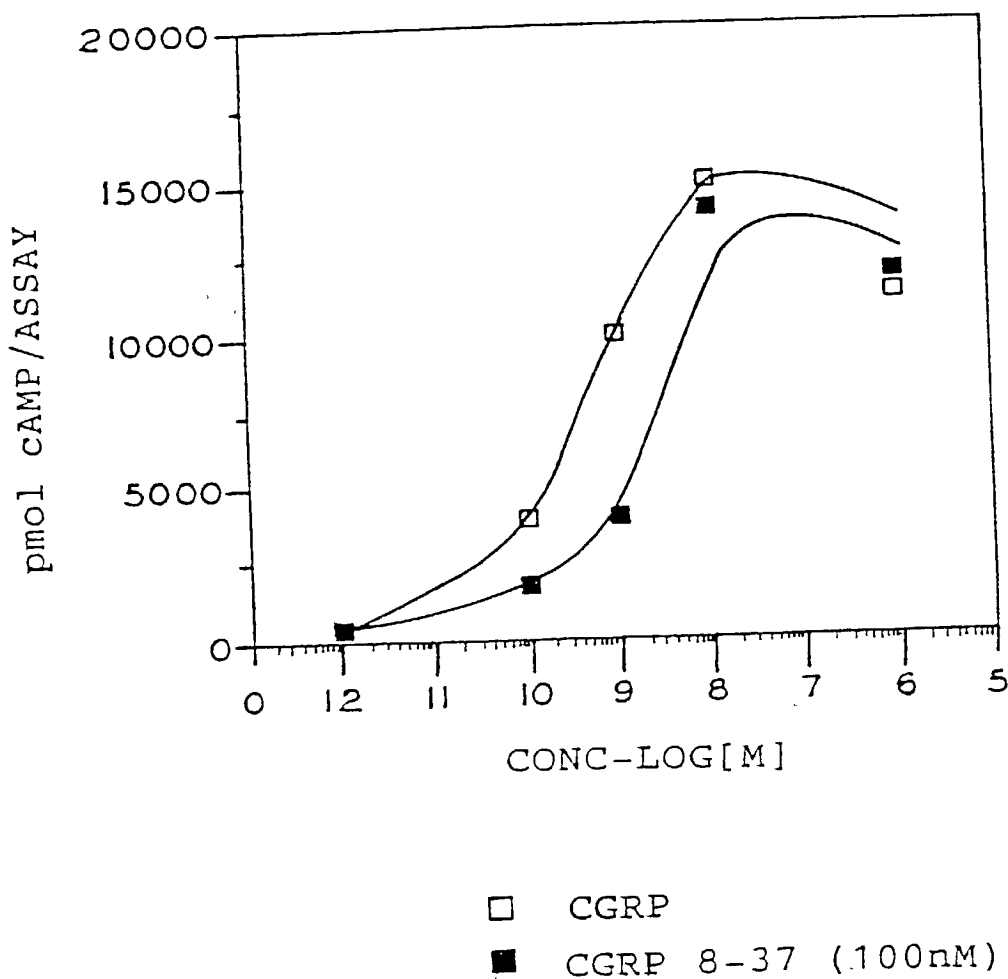
EFFECT OF CGRP TREATMENT OF 293  
CELL LINES STABLY TRANSFORMED  
WITH THE pCDNHCGRP $\alpha$  CONSTRUCT





# FIG. 7

EFFECT OF CGRP8-37 ON CGRP-MEDIATED  
cAMP IN pCDNHCGRPr STABLY  
TRANSFORMED 293 CELLS (CLONE 22)





[125I]CGRP BINDING TO pCDNHCGPr TRANSFORMED  
293 CELLS (CLONE 22) MEMBRANES

FIG. 8A

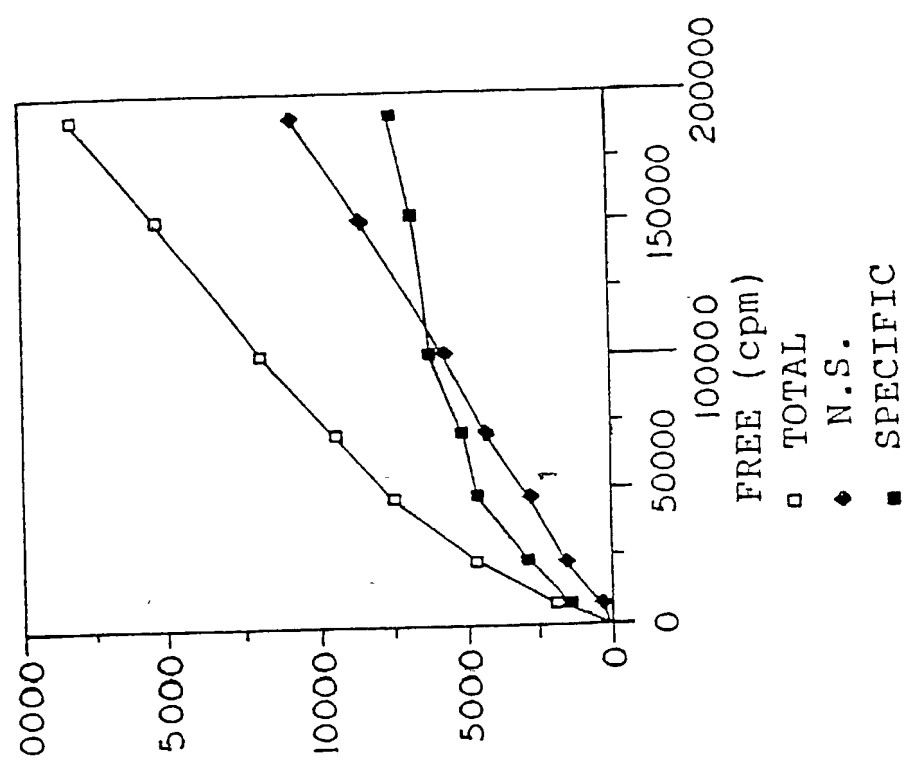
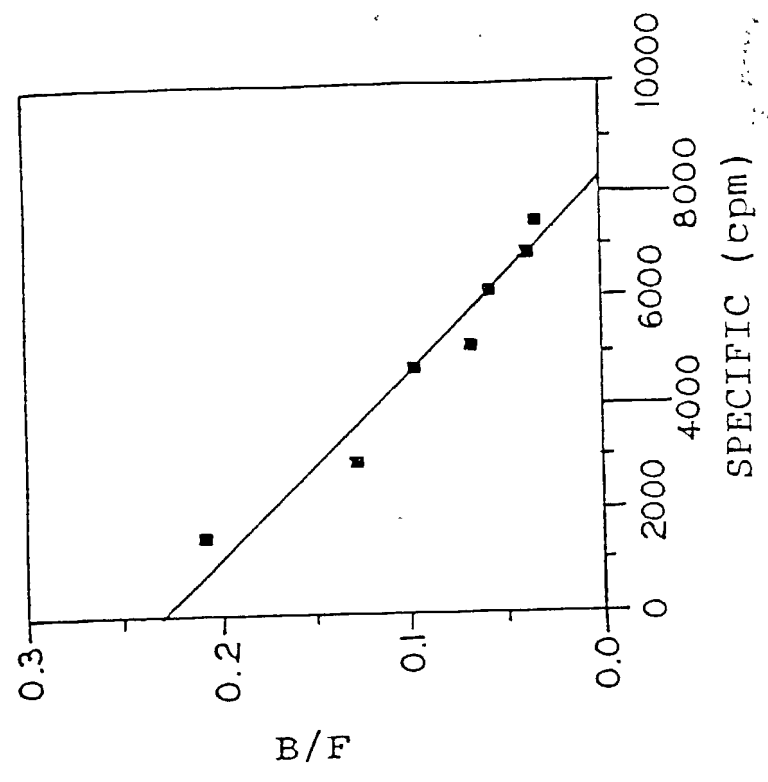
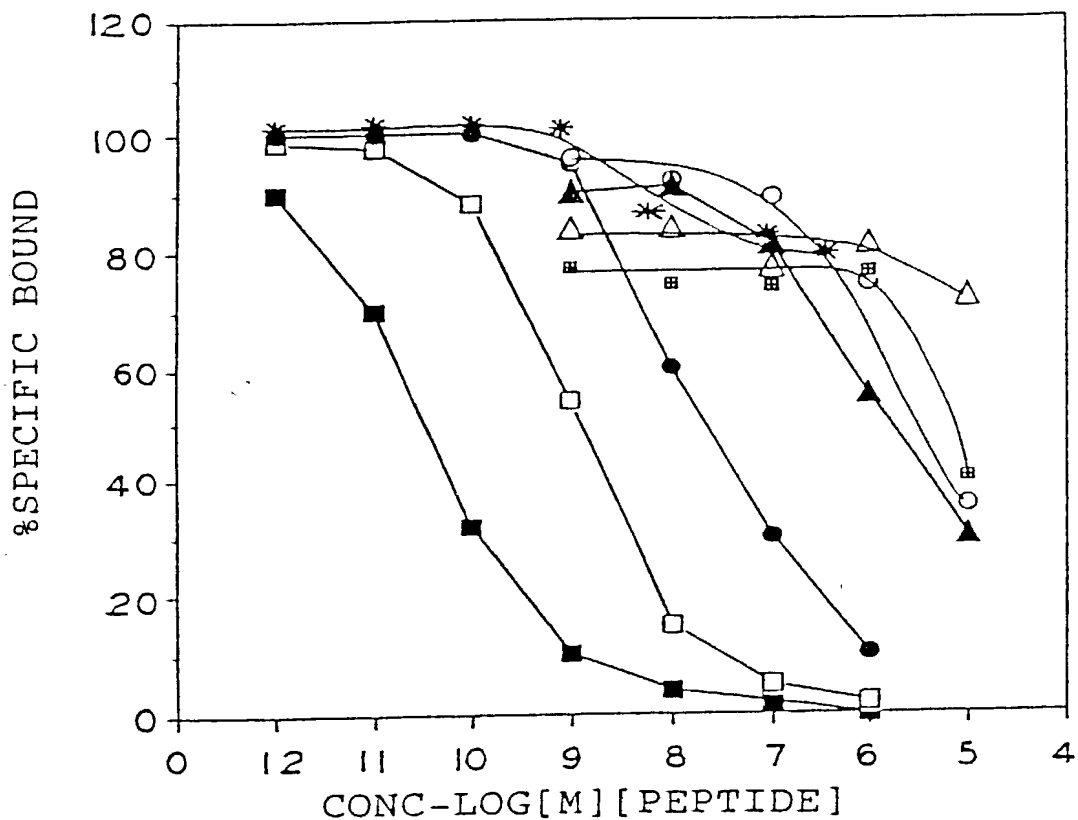


FIG. 8B



# FIG. 9

COMPETITION CURVES FOR  
REPRESENTATIVE CGRP ANALOGS AGAINST  
[125I]CGRP BINDING IN pCDNHCGRP $\alpha$   
TRANSFORMED CELL (CLONE22) MEMBRANES



CGRP>CGRP8-37>ADM>sCT8-32>sCT>VIP>Amylin,LCT

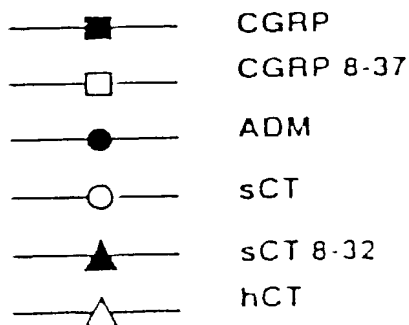




FIG. 10B

MATCH WITH FIG. 10A

201 KMF~~LT~~YILNSMIIIIHLVEVPNGELVRRDPVSKILHFFHQYMMACNY 250  
228 FWMLCEGIY~~LH~~TLIVVAVFAEKQHLMWYF~~LG~~WGFFLIPACIHAIARSLY 277  
251 FWMLCEGIY~~LH~~TLIVVAVFTEKQRLRWYLLGWGFFLVPTTIIHAITRAVY 300  
278 YDNCWISSD~~TH~~LLYIIHGPICAALLVNLFLLNIVRVLITKLKVTHQAE 327  
301 FDN~~CW~~LSVETHLLYIIHG~~PV~~MAALVNVFF~~LL~~NIVRVLVTKMRETHEAE 350  
328 SNLYMKAVRATLILVPLLGI~~EF~~VLIPWRPEGKIAEEVYDYIMHILMHFQG 377  
351 SHMYLKAVKATMILV~~PL~~LLGIQFVFPWRPSNKMGLKIDYVMHSLIHFGQ 400  
378 LLVSTIFCFFNGEVQAILRRNWNQYKIQFGNSFSNSEALRSASYTVSTIS 427  
401 FFVAT~~IY~~CFCNNEVQTTVKRQWAQFKIQWNQWRGRRPSNRSARAAAAAE 450  
428 DGPYSHDCPSEHLNGKS.IHDIENVLKPENLYN.... 461  
451 AGDIPYICHQEPRNEPANNQGEESA~~EII~~PLNIEQESSA 490

490 33 465 465 465 465

# FIG. 11A Comparison of Human and Rat CGRP Receptor Amino Acid Sequences

```

1 .MEKKCTLYFLVLLPFFMILVTAEELESPEDSIQLGVTRNKIMTAQYECY 49
  |:|||||:|:|:| | | | | | | | | | | | | | | | | | | | | | |
1 MMDKKCTLCFLFLLNLMALIAESEEKANQT.DLGVTRNKIMTAQYECY 49

50 QKIMQDPIQQAEGVYCNRTWDGWLWCWNDVAAGTESMQLCPDYFQDFDPSE 99
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
50 QKIMQDPIQQGEGLYCNRTWDGWLWCWNDVAAGTESMQLCPDYFQDFDPSE 99

100 KVTKICDQDGNWFRHPASNRTWTNYTQCNVNTHKVKTALNLFYLTIGH 149
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
100 KVTKICDQDGNWFRHPDSNRTWTNYTLCNNSTHEKEKTALNLFYLTIGH 149

150 GLSIASLLISLGIFFFYFKSLSCQRITLHKNLFFSFVCNSVVTIIHLTAVA 199
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
150 GLSIASLLIISLIIFFFYFKSLSCQRITLHKNLFFSFVCNSIVTIIHLTAVA 199

200 NNQALVATNPVSCKVSQFIHLYLMGCNYFWMLCEGIYLTIVVAVFAEK 249
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
200 NNQALVATNPVSCKVSQFIHLYLMGCNYFWMLCEGIYLTIVVAVFAEK 249

```

MATCH WITH FIG. 11B

49 99 149 199 249

FIG. 11B

**MATCH WITH FIG. 11A**

250 QHLMWYFLGWGFLLPACIHAIARSLYYNDNCWISSDTHLLYIIHGPI 299  
 250 QHLMWYFLGWGFLLPACIHAIARSLYYNDNCWISSDTHLLYIIHGPI 299  
 300 AALLVNLFLLNIVRVLITKLKVTHQAESNLYMKAVRATLILVPLLGIEF 349  
 300 AALLVNLFLLNIVRVLITKLKVTHQAESNLYMKAVRATLILVPLLGIEF 349  
 350 VLIWRPECKIAEEVYDYMILMHFQGLLVSTIFCFNGEVQAILRRNW 399  
 350 VLFWRPECKVAEEVYDYMILMHYQGLLVSTIFCFNGEVQAILRRNW 399  
 400 NOYKIQFGNSFNSALRSASYTVSTISDGPYSHDCPSEHLNGKSIHDI 449  
 400 NOYKIQFGNGFSDALRSASYTVSTISDVQGYSHDCPTEHLNGKSIQDI 449  
 450 ENVLLKPENLYN... 461  
 450 ENVALKPEKMYDLVM 464

all other things being equal, all men are more likely to